Amendments to the Specification

Please replace paragraph **[0001]** with the following amended paragraph:

[0001] This application is a continuation of U.S. Patent Application Serial No. 09/147,875, now U.S. Patent No. 6,638,516, which is a continuation-in-part ("CIP") of ~~USSN~~ U.S. Patent Application Serial No. 08/710,749, filed September 20, 1996, now U.S. Patent No. 5,955,089, and a U.S. National Application of PCT Application No. PCT/US97/16761, filed September 22, 1997, all of which are incorporated herein by their entirety.

Please replace paragraph **[0002]** with the following amended paragraph:

[0002] The *Streptococcus* ~~pneumoniae~~ *pneumoniae* strain designated Rx1 has been deposited pursuant to, and in satisfaction of, the requirements of the Budapest Treaty on the International Recognition of The Deposit of Microorganisms for The Purposes of Patent Procedure, with the American Type Culture Collection (ATCC), now at 10801 University Boulevard, Manassas, VA 20110-2209, under ATCC Accession No. 55834, on October 3, 1996.

Please replace paragraph **[0029]** with the following amended paragraph:

[0029] The invention provides vaccine compositions, wherein the families further comprise one or more clades. Clades are defined by PspAs having ~~at least~~ greater than 75% homology ~~with other PspAs from a strain within the clade~~ in the aligned sequences of the C-terminal region of the alpha helix of PspA.

Please replace paragraph **[0103]** with the following amended paragraph:

[0103] Approximately 36% of all strains examined were serotyped as clade 2, 22% as clade 3 and 23% as clade 4. A vaccine comprised of PspAs from these three clades alone would cover greater than 80% of the *S. pneumoniae* strains examined (Table 11). Of the 437 strains examined, 98.4% of these strains could be serotyped into one of the six clades, again demonstrating the potential for a finite number of vaccine components, based on clade-specific PspAs, to confer broad immunity against infection caused by *S. pneumoniae* (Table 11). In fact, based on the high degree of cross-reactivity within families, a vaccine

composition comprised of a single representative member of each family should confer such immunity.

Please replace the paragraph in the Abstract of the Disclosure section on page 43 with the following amended paragraph:

The present invention relates to vaccine composition(s) comprising at least two PspAs from strains selected from at least one family, the family being defined by PspAs from strains belonging to the family having greater than or equal to 50% homology in aligned sequences of a C-terminal region of an alpha helical region of PspA. Additionally, the families are further comprised of clades, wherein PspAs from strains which belong to a clade exhibit ~~at least~~ greater than 75% sequence homology in aligned sequences of the C-terminal region of the alpha helix of PspA. Vaccine compositions of the present invention preferably comprise a minimum of 4 and a maximum of 6 strains representing a single clade each, and the at least two PspAs are optionally serologically or broadly cross-reactive.